



## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Boyle, William J.
- (ii) TITLE OF INVENTION: Osteoprotegerin Binding Proteins
- (iii) NUMBER OF SEQUENCES: 39
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Amgen Inc.
  - (B) STREET: One Amgen Center Drive
  - (C) CITY: Thousand Oaks
  - (D) STATE: California
  - (E) COUNTRY: USA
  - (F) ZIP: 91320-1789
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Winter, Robert B.
  - (C) REFERENCE/DOCKET NUMBER: A-451F

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Asp Pro Asn Arg Gln Asp Ile Asp  
1 5

## (2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 52 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GTTCTCCTCA TATGGATCCA AACCGTATTT CTGAAGACAG CACTCACTGC TT

52

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TACGCACTCC GCGGTTAGTC TATGTCCTGA ACTTTGA

37

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Glu Asn Ala Gly Gln Asp Ile Asp  
1 5

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 51 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATTTGATTCT AGAAGGAGGA ATAACATATG CATGAAAACG CAGGTCTGCA G

51

## (2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 42 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TATCCGCGGA TCCTCGAGTT AGTCTATGTC CTGAAC TTG AA

42

## (2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 8 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Glu Asp Thr Leu Gln Asp Ile Asp  
 1 5

## (2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATTTGATTCT AGAAGGAGGA ATAACATATG TCTGAAGACA CTCTGCCGGA CTCC

54

## (2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 9 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

B1  
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Lys Gln Ala Phe Gln Gln Asp Ile Asp  
1 5

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 48 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATTTGATTCT AGAAGGAGGA ATAACATATG AAACAAGCTT TTCAGGGG

48

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Lys Glu Leu Gln His Gln Asp Ile Asp  
1 5 10

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 51 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATTTGATTCT AGAAGGAGGA ATAACATATG AAAGAACTGC AGCACATTGT G

51

## (2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met	Gln	Arg	Phe	Ser	Gly	Gln	Asp	Ile	Asp
1				5					10

## (2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 51 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATTTGATTCT AGAAGGAGGA ATAACATATG CAGCGTTTCT CTGGTGCTCC A

51

## (2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 9 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met	Glu	Gly	Ser	Trp	Gln	Asp	Ile	Asp
1				5				

## (2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 40 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GTTCTCCTCA TATGGAAGGT TCTTGTTGG ATGTGGCCCA

40

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 9 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met Arg Gly Lys Pro Gln Asp Ile Asp  
1 5

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 44 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GTTCTCCTCA TATGCGTGGT AAACCTGAAG CTCAACCATT TGCA

44

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 9 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Lys Pro Glu Ala Gln Asp Ile Asp  
1 5

## (2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 53 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GTTCTCCTCA TATGAAACCT GAAGCTCAAC CATTTGCACA CCTCACCATC AAT

53

## (2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 9 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met His Leu Thr Ile Gln Asp Ile Asp  
1 5

## (2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 65 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GTTCTCCTCA TATGCATTTA ACTATTAACG CTGCATCTAT CCCATCGGGT TCCCATAAAG  
TCACT

60

65

## (2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 9 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met Thr Ile Asn Ala Gln Asp Ile Asp  
1 5

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GTTCTCCTCA TATGACTATT AACGCTGCAT CTATCCCATC GGGTTCCCAT AAAGTCACT

59

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Met Lys Pro Glu Ala Gln Pro Phe Ala His  
1 5 10

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CCTCTAGGCC TGTACTTTCG AGCGCAGATG

30



## (2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CCTCTGCGGC CGCGTCTATG TCCTGAACTT TG

32

## (2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 46 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CCTCTCTCGA GTGGACAACC CAGAAGCCTG AGGCCCAGCC ATTTGC

46

## (2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CCTCTGCGGC CGCGTCTATG TCCTGAACTT TG

32

## (2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 56 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

AGCTTCCACC ATGAACAAGT GGCTGTGCTG CGCACTCCTG GTGCTCCTGG ACATCA

56

## (2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 56 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TCGATGATGT CCAGGAGCAC CAGGAGTGCG CAGCACAGCC ACTTGTCAT GGTGGA

56

## (2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Asn	Ala	Ala	Ser	Ile	Pro	Ser	Gly	Ser	His	Lys	Val	Thr	Leu	Ser	Ser
1				5					10					15	
Trp	Tyr	His	Asp	Arg	Gly	Trp	Ala	Lys	Ile	Ser					
			20					25							

## (2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Asn	Ala	Ala	Ser	Ile	Pro	Ser	Gly	Ser	His	Lys	Val	Thr	Leu	Ser	Ser
1				5					10					15	
Trp	Tyr	His	Asp	Arg	Gly	Trp	Ala	Lys	Ile	Ser	Cys				
			20					25							

## (2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 17 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Val Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu  
 1                      5                      10                      15  
 Met

## (2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 18 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Val Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu  
 1                      5                      10                      15  
 Met Cys

## (2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2295 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 158..1105

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GAGCTCGGAT CCACTACTCG ACCACGCGT CCGGCCAGGA CCTCTGTGAA CCGGTCGGGG                      60  
 CGGGGGCCGC CTGGCCGGGA GTCTGCTCGG CGGTGGGTGG CCGAGGAAGG GAGAGAACGA                      120

TCGCGGAGCA GGGCGCCCCGA ACTCCGGGGCG CCGCGCC																ATG Met 1	CGC Arg	CGG Arg	GCC Ala	AGC Ser 5	CGA Arg	175
GAC Asp	TAC Tyr	GGC Gly	AAG Lys 10	TAC Tyr	CTG Leu	CGC Arg	AGC Ser	TCG Ser 15	GAG Glu	GAG Glu	ATG Met	GGC Gly	AGC Ser 20	GGC Gly	CCC Pro	223						
GGC Gly	GTC Val	CCA Pro 25	CAC His	GAG Glu	GGT Gly	CCG Pro	CTG Leu 30	CAC His	CCC Pro	GCG Ala	CCT Pro	TCT Ser 35	GCA Ala	CCG Pro	GCT Ala	271						
CCG Pro	GCG Ala 40	CCG Pro	CCA Pro	CCC Pro	GCC Ala	GCC Ala 45	TCC Ser	CGC Arg	TCC Ser	ATG Met	TTC Phe 50	CTG Leu	GCC Ala	CTC Leu	CTG Leu	319						
GGG Gly 55	CTG Leu	GGA Gly	CTG Leu	GGC Gly	CAG Gln 60	GTG Val	GTC Val	TGC Cys	AGC Ser	ATC Ile 65	GCT Ala	CTG Leu	TTC Phe	CTG Leu	TAC Tyr 70	367						
TTT Phe	CGA Arg	GCG Ala	CAG Gln	ATG Met 75	GAT Asp	CCT Pro	AAC Asn	AGA Arg	ATA Ile 80	TCA Ser	GAA Glu	GAC Asp	AGC Ser	ACT Thr 85	CAC His	415						
TGC Cys	TTT Phe	TAT Tyr	AGA Arg 90	ATC Ile	CTG Leu	AGA Arg	CTC Leu	CAT His 95	GAA Glu	AAC Asn	GCA Ala	GGT Gly	TTG Leu 100	CAG Gln	GAC Asp	463						
TCG Ser	ACT Thr	CTG Leu 105	GAG Glu	AGT Ser	GAA Glu	GAC Asp	ACA Thr 110	CTA Leu	CCT Pro	GAC Asp	TCC Ser	TGC Cys 115	AGG Arg	AGG Arg	ATG Met	511						
AAA Lys	CAA Gln	GCC Ala	TTT Phe	CAG Gln	GGG Gly	GCC Ala 125	GTG Val	CAG Gln	AAG Lys	GAA Glu	CTG Leu	CAA Gln	CAC His	ATT Ile	GTG Val	559						
GGG Gly 135	CCA Pro	CAG Gln	CGC Arg	TTC Phe	TCA Ser	GGA Gly	GCT Ala	CCA Pro	GCT Ala	ATG Met	ATG Met	GAA Glu	GGC Gly	TCA Ser	TGG Trp 150	607						
TTG Leu	GAT Asp	GTG Val	GCC Ala	CAG Gln 155	CGA Arg	GGC Gly	AAG Lys	CCT Pro	GAG Glu	GCC Ala	CAG Gln	CCA Pro	TTT Phe	GCA Ala	CAC His	655						
CTC Leu	ACC Thr	ATC Ile	AAT Asn 170	GCT Ala	GCC Ala	AGC Ser	ATC Ile	CCA Pro 175	TCG Ser	GGT Gly	TCC Ser	CAT His	AAA Lys	GTC Val	ACT Thr	703						
CTG Leu	TCC Ser	TCT Ser	TGG Trp	TAC Tyr	CAC His	GAT Asp	CGA Arg	GGC Gly	TGG Trp	GCC Ala	AAG Lys	ATC Ile	TCT Ser	AAC Asn	ATG Met	751						
ACG Thr	TTA Leu	AGC Ser	AAC Asn	GGA Gly	AAA Lys	CTA Leu	AGG Arg	GTT Val	AAC Asn	CAA Gln	GAT Asp	GGC Gly	TTC Phe	TAT Tyr	TAC Tyr	799						
CTG Leu	TAC Tyr	GCC Ala	AAC Asn	ATT Ile	TGC Cys	TTT Phe	CGG Arg	CAT His	CAT His	GAA Glu	ACA Thr	TCG Ser	GGA Gly	AGC Ser	GTA Val	847						
CCT Pro	ACA Thr	GAC Asp	TAT Tyr	CTT Leu	CAG Gln	CTG Leu	ATG Met	GTG Val	TAT Tyr	GTC Val	GTT Val	AAA Lys	ACC Thr	AGC Ser	ATC Ile	895						

AAA ATC CCA AGT TCT CAT AAC CTG ATG AAA GGA GGG AGC ACG AAA AAC	943
Lys Ile Pro Ser Ser His Asn Leu Met Lys Gly Gly Ser Thr Lys Asn	
250 255 260	
TGG TCG GGC AAT TCT GAA TTC CAC TTT TAT TCC ATA AAT GTT GGG GGA	991
Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly	
265 270 275	
TTT TTC AAG CTC CGA GCT GGT GAA GAA ATT AGC ATT CAG GTG TCC AAC	1039
Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser Ile Gln Val Ser Asn	
280 285 290	
CCT TCC CTG CTG GAT CCG GAT CAA GAT GCG ACG TAC TTT GGG GCT TTC	1087
Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe	
295 300 305 310	
AAA GTT CAG GAC ATA GAC TGAGACTCAT TTCGTGGAAC ATTAGCATGG	1135
Lys Val Gln Asp Ile Asp	
315	
ATGTCCTAGA TGTTTGGAAA CTTCTTAAAA AATGGATGAT GTCTATACAT GTGTAAGACT	1195
ACTAAGAGAC ATGGCCACG GTGTATGAAA CTCACAGCCC TCTCTCTTGA GCCTGTACAG	1255
GTTGTGTATA TGTAAGTCC ATAGGTGATG TTAGATTCAT GGTGATTACA CAACGGTTTT	1315
ACAATTTTGT AATGATTTCC TAGAATTGAA CCAGATTGGG AGAGGTATTC CGATGCTTAT	1375
GAAAACTTA CACGTGAGCT ATGGAAGGGG GTCACAGTCT CTGGGTCTAA CCCCTGGACA	1435
TGTGCCACTG AGAACCTTGA AATTAAGAGG ATGCCATGTC ATTGCAAAGA AATGATAGTG	1495
TGAAGGGTTA AGTTCTTTTG AATTGTTACA TTGCGCTGGG ACCTGCAAAT AAGTTCTTTT	1555
TTTCTAATGA GGAGAGAAAA ATATATGTAT TTTTATATAA TGTCTAAAGT TATATTTTCAG	1615
GTGTAATGTT TTCTGTGCAA AGTTTTGTAA ATTATATTTG TGCTATAGTA TTTGATTCAA	1675
AATATTTAAA AATGTCTCAC TGTTGACATA TTTAATGTTT TAAATGTACA GATGTATTTA	1735
ACTGGTGAC TTTGTAATTC CCCTGAAGGT ACTCGTAGCT AAGGGGGCAG AATACTGTTT	1795
CTGGTGACCA CATGTAGTTT ATTTCTTTTAT TCTTTTAAAC TTAATAGAGT CTTCAGACTT	1855
GTCAAAACTA TGCAAGCAAA ATAAATAAAT AAAAATAAAA TGAATACCTT GAATAATAAG	1915
TAGGATGTTG GTCACCAGGT GCCTTTCAAA TTTAGAAGCT AATTGACTTT AGGAGCTGAC	1975
ATAGCCAAAA AGGATACATA ATAGGCTACT GAAATCTGTC AGGAGTATTT ATGCAATTAT	2035
TGAACAGGTG TCTTTTTTTA CAAGAGCTAC AAATTGTAAA TTTTGTTTCT TTTTTTTCCC	2095
ATAGAAAATG TACTATAGTT TATCAGCCAA AAAACAATCC ACTTTTTAAT TTAGTGAAAG	2155
TTATTTTATT ATACTGTACA ATAAAAGCAT TGTCTCTGAA TGTTAATTTT TTGGTACAAA	2215
AAATAAATTT GTACGAAAAC CTGAAAAAAA AAAAAAAAAA AAAAAAAGG GCGGCCGCTC	2275
TAGAGGGCCC TATTCTATAG	2295

## (2) INFORMATION FOR SEQ ID NO:37:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 316 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

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Met Arg Arg Ala Ser Arg Asp Tyr Gly Lys Tyr Leu Arg Ser Ser Glu
 1          5          10          15
Glu Met Gly Ser Gly Pro Gly Val Pro His Glu Gly Pro Leu His Pro
          20          25          30
Ala Pro Ser Ala Pro Ala Pro Ala Pro Pro Pro Ala Ala Ser Arg Ser
          35          40          45
Met Phe Leu Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser
          50          55          60
Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile
 65          70          75          80
Ser Glu Asp Ser Thr His Cys Phe Tyr Arg Ile Leu Arg Leu His Glu
          85          90          95
Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro
          100          105          110
Asp Ser Cys Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val Gln Lys
          115          120          125
Glu Leu Gln His Ile Val Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala
          130          135          140
Met Met Glu Gly Ser Trp Leu Asp Val Ala Gln Arg Gly Lys Pro Glu
          145          150          155          160
Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser
          165          170          175
Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp
          180          185          190
Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn
          195          200          205
Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His
          210          215          220
Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr
          225          230          235          240
Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys
          245          250          255
Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr
          260          265          270
Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile
          275          280          285

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Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala  
 290 295 300

Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp  
 305 310 315

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2272 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 185..1135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

AAGCTTGGTA CCGAGCTCGG ATCCACTACT CGACCCACGC GTCCGCGCGC CCCAGGAGCC	60
AAAGCCGGGC TCCAAGTCGG CGCCCCACGT CGAGGCTCCG CCGCAGCCTC CGGAGTTGGC	120
CGCAGACAAG AAGGGGAGGG AGCGGGAGAG GGAGGAGAGC TCCGAAGCGA GAGGGCCGAG	180
CGCC ATG CGC CGC GCC AGC AGA GAC TAC ACC AAG TAC CTG CGT GGC TCG	229
Met Arg Arg Ala Ser Arg Asp Tyr Thr Lys Tyr Leu Arg Gly Ser	15
1 5 10	
GAG GAG ATG GGC GGC GGC CCC GGA GCC CCG CAC GAG GGC CCC CTG CAC	277
Glu Glu Met Gly Gly Gly Pro Gly Ala Pro His Glu Gly Pro Leu His	30
20 25	
GCC CCG CCG CCG CCT GCG CCG CAC CAG CCC CCC GCC GCC TCC CGC TCC	325
Ala Pro Pro Pro Pro Ala Pro His Gln Pro Pro Ala Ala Ser Arg Ser	45
35 40	
ATG TTC GTG GCC CTC CTG GGG CTG GGG CTG GGC CAG GTT GTC TGC AGC	373
Met Phe Val Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser	60
50 55	
GTC GCC CTG TTC TTC TAT TTC AGA GCG CAG ATG GAT CCT AAT AGA ATA	421
Val Ala Leu Phe Phe Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile	75
65 70	
TCA GAA GAT GGC ACT CAC TGC ATT TAT AGA ATT TTG AGA CTC CAT GAA	469
Ser Glu Asp Gly Thr His Cys Ile Tyr Arg Ile Leu Arg Leu His Glu	95
80 85 90	
AAT GCA GAT TTT CAA GAC ACA ACT CTG GAG AGT CAA GAT ACA AAA TTA	517
Asn Ala Asp Phe Gln Asp Thr Thr Leu Glu Ser Gln Asp Thr Lys Leu	110
100 105	
ATA CCT GAT TCA TGT AGG AGA ATT AAA CAG GCC TTT CAA GGA GCT GTG	565
Ile Pro Asp Ser Cys Arg Arg Ile Lys Gln Ala Phe Gln Gly Ala Val	125
115 120	

CAA AAG GAA TTA CAA CAT ATC GTT GGA TCA CAG CAC ATC AGA GCA GAG Gln Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg Ala Glu 130 135 140	613
AAA GCG ATG GTG GAT GGC TCA TGG TTA GAT CTG GCC AAG AGG AGC AAG Lys Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg Ser Lys 145 150 155	661
CTT GAA GCT CAG CCT TTT GCT CAT CTC ACT ATT AAT GCC ACC GAC ATC Leu Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr Asp Ile 160 165 170 175	709
CCA TCT GGT TCC CAT AAA GTG AGT CTG TCC TCT TGG TAC CAT GAT CGG Pro Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg 180 185 190	757
GGT TGG GCC AAG ATC TCC AAC ATG ACT TTT AGC AAT GGA AAA CTA ATA Gly Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile 195 200 205	805
GTT AAT CAG GAT GGC TTT TAT TAC CTG TAT GCC AAC ATT TGC TTT CGA Val Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg 210 215 220	853
CAT CAT GAA ACT TCA GGA GAC CTA GCT ACA GAG TAT CTT CAA CTA ATG His His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met 225 230 235	901
GTG TAC GTC ACT AAA ACC AGC ATC AAA ATC CCA AGT TCT CAT ACC CTG Val Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr Leu 240 245 250 255	949
ATG AAA GGA GGA AGC ACC AAG TAT TGG TCA GGG AAT TCT GAA TTC CAT Met Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His 260 265 270	997
TTT TAT TCC ATA AAC GTT GGT GGA TTT TTT AAG TTA CGG TCT GGA GAG Phe Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser Gly Glu 275 280 285	1045
GAA ATC AGC ATC GAG GTC TCC AAC CCC TCC TTA CTG GAT CCG GAT CAG Glu Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln 290 295 300	1093
GAT GCA ACA TAC TTT GGG GCT TTT AAA GTT CGA GAT ATA GAT Asp Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp Ile Asp 305 310 315	1135
TGAGCCCCAG TTTTGGAGT GTTATGTATT TCCTGGATGT TTGGAAACAT TTTTAAAC	1195
AAGCCAAGAA AGATGTATAT AGGTGTGTGA GACTACTAAG AGGCATGGCC CCAACGGTAC	1255
ACGACTCAGT ATCCATGCTC TTGACCTTGT AGAGAACACG CGTATTTACA GCCAGTGGGA	1315
GATGTTAGAC TCATGGTGTG TTACACAATG GTTTTTTAAAT TTTGTAATGA ATTCTAGAA	1375
TTAAACCAGA TTGGAGCAAT TACGGGTGTA CCTTATGAGA AACTGCATGT GGGCTATGGG	1435
AGGGGTGGT CCCTGGTCAT GTGCCCCTTC GCAGCTGAAG TGGAGAGGGT GTCATCTAGC	1495
GCAATTGAAG GATCATCTGA AGGGGCAAAT TCTTTTGAAT TGTTACATCA TGCTGGAACC	1555
TGCAAAAAAT ACTTTTTCTA ATGAGGAGAG AAAATATATG TATTTTATA TAATATCTAA	1615



B1  
Cont.

AGTTATATTT CAGATGTAAT GTTTTCTTTG CAAAGTATTG TAAATTATAT TTGTGCTATA	1675
GTATTTGATT CAAAATATTT AAAAATGTCT TGCTGTTGAC ATATTTAATG TTTTAAATGT	1735
ACAGACATAT TTAACGGTG CACTTTGTAA ATTCCCTGGG GAAAACTTGC AGCTAAGGAG	1795
GGGAAAAAAA TGTGTGTTCC TAATATCAAA TGCAGTATAT TTCTTCGTTC TTTTAAAGTT	1855
AATAGATTTT TTCAGACTTG TCAAGCCTGT GCAAAAAAAT TAAAATGGAT GCCTTGAATA	1915
ATAAGCAGGA TGTGGGCCAC CAGGTGCCTT TCAAATTTAG AAACCTAATTG ACTTTAGAAA	1975
GCTGACATTG CCAAAAAGGA TACATAATGG GCCACTGAAA TCTGTCAAGA GTAGTTATAT	2035
AATTGTTGAA CAGGTGTTTT TCCACAAGTG CCGCAAATTG TACCTTTTTT TTTTTTCAA	2095
AATAGAAAAG TTATTAGTGG TTTATCAGCA AAAAAGTCCA ATTTTAATTT AGTAAATGTT	2155
ATCTTATACT GTACAATAAA AACATTGCCT TTGAATGTTA ATTTTTTGGT ACAAAAATAA	2215
ATTTATATGA AAAAAAAAAA AAAAGGGCGG CCGCTCTAGA GGGCCCTATT CTATAGG	2272

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Met	Arg	Arg	Ala	Ser	Arg	Asp	Tyr	Thr	Lys	Tyr	Leu	Arg	Gly	Ser	Glu	1	5	10	15
Glu	Met	Gly	Gly	Gly	Pro	Gly	Ala	Pro	His	Glu	Gly	Pro	Leu	His	Ala	20	25	30	
Pro	Pro	Pro	Pro	Ala	Pro	His	Gln	Pro	Pro	Ala	Ala	Ser	Arg	Ser	Met	35	40	45	
Phe	Val	Ala	Leu	Leu	Gly	Leu	Gly	Leu	Gly	Gln	Val	Val	Cys	Ser	Val	50	55	60	
Ala	Leu	Phe	Phe	Tyr	Phe	Arg	Ala	Gln	Met	Asp	Pro	Asn	Arg	Ile	Ser	65	70	75	80
Glu	Asp	Gly	Thr	His	Cys	Ile	Tyr	Arg	Ile	Leu	Arg	Leu	His	Glu	Asn	85	90	95	
Ala	Asp	Phe	Gln	Asp	Thr	Thr	Leu	Glu	Ser	Gln	Asp	Thr	Lys	Leu	Ile	100	105	110	
Pro	Asp	Ser	Cys	Arg	Arg	Ile	Lys	Gln	Ala	Phe	Gln	Gly	Ala	Val	Gln	115	120	125	
Lys	Glu	Leu	Gln	His	Ile	Val	Gly	Ser	Gln	His	Ile	Arg	Ala	Glu	Lys	130	135	140	
Ala	Met	Val	Asp	Gly	Ser	Trp	Leu	Asp	Leu	Ala	Lys	Arg	Ser	Lys	Leu	145	150	155	160

Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr Asp Ile Pro  
 165 170 175  
 Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg Gly  
 180 185 190  
 Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile Val  
 195 200 205  
 Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His  
 210 215 220  
 His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met Val  
 225 230 235 240  
 Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr Leu Met  
 245 250 255  
 Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His Phe  
 260 265 270  
 Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser Gly Glu Glu  
 275 280 285  
 Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp  
 290 295 300  
 Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp Ile Asp  
 305 310 315

B1  
 Conclude